

REPLACEMENT FIG. 1

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
x_dropoff: 15 expect: 10.0 wordsize: 3 Filter: []

Sequence 1 lcl|seq_1 Length 510 (1..510)

Sequence 2 lcl|seq_2 Length 512 (1..512)

2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0
Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

Query: 1	MFIESFRVESPHVRYGAAEIESDYQYDTTEL VHESH DGASRWIVRPKSVRYNFR TTTTVP	SEQ ID2
60		
	MFIESFRVESPHVRYGAAEIES+Y+YDTTEL VHESH DGASRW+VRPKSV+Y+ERT+TTVP	
Sbjct: 1	MFIESFRVESPHVRYGAAEIESEYRYDTTEL VHESH DGASRWVVRPKSVQXHFR TSTTVP	SEQ ID3
60		
Query: 61	KLGVMLVGWGGNNGSTLTAGVIANREGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE	SEQ ID2
120		
	KLGVMLVGWGGNNGSTLTAGVIA+REGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE	
Sbjct: 61	KLGVMLVGWGGNNGSTLTAGVIASREGISWATKDKVQQANYYGSLTQASTIRVGSYNGEE	SEQ ID3
120		
Query: 121	IYAPFKSLLPMVNPDDLVEGGWDISNMNLADAMTRAKVLDIDLQQLRPYMES-----	SEQ ID2
173		
	IYAPFKSLLPMVNPDDLEVEGGWDISNMNLADAMTRAKVLDIDLQQLRPYMES	
Sbjct: 121	IYAPFKSLLPMVNPDDLVEGGWDISNMNLADAMTRAKVLDIDLQQLRPYMESWCLSLAS	SEQ ID3
180		
Query: 174	MVPL--PGIYDPDVIAANQGSRANNVIKGTKKEQMEQIIKDIREFKEKSKVDKVVVLWTA	SEQ ID2
231		
	M+P . P DP A SR ++ + + KDIREFKE +K+DK VVIWTA	
Sbjct: 181	MIPTSSPLTRDP---ARTMSSRE-----PRRSRWGRSSKDIREFKENNKMDKAVVWTA	SEQ ID3
231		

Fig: 1

Query: 232 NTERYSN-VCVGLNDTHENLLASVDKHEAEISPSTLYAIACV-MEGIPFIHGS PQNTFVP SEQ ID2
289
NTERY+H 4C+GL T ASVD+H4AEISPSTLY IEG+ I G+ + P
Sbjct: 232 NTERYNNCLCLGLM-TNGKPSASVDRNQAEISPSTLYCHCLASLEGVRSITGALKKKSWP SEQ ID3
290

Query: 290 GLIDLAIKNNCLI-GGDDFKSGQTKMKSVLVDLVLGAGIKPTSIVSYNHLGNNIDGMNLSA SEQ ID2
348
G+ DLAIK GG K G+ K K+ LVDL+GAGIKPTSIVSYNHLGNNIDG NLSA
Sbjct: 291 GIDDLAIKKKLDPGGLIQKRGKPKKKTGLVDL+GAGIKPTSIVSYNHLGNNIDGMNLSA SEQ ID3
350

Query: 349 PQFRSKEISKSNVDDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTS EIFM SEQ ID2
408
PQFRSKEISKS+VDDMVSSNAILYE GEHPDHVVVIKYVPYVGDSKRAMDEYTS EIFM
Sbjct: 351 PQFRSKEISKSSVDDMVSSNAILYEPGEHPDHVVVIKYVPYVGDSKRAMDEYTS EIFM SEQ ID3
410

Query: 409 GGGKSTIVLHNTCEDSLAAPIILDVLVLAELSTRIQLKAEGERKFSFHPVATILSYLTK SEQ ID2
468
GGK+TIVLHNTCEDSLAAPIILDVLVLAELSTRIQLK EGEEKFHSFHPVATILSYLTK
Sbjct: 411 GGGKSTIVLHNTCEDSLAAPIILDVLVLAELSTRIQLKAEGERKFSFHPVATILSYLTK SEQ ID3
470

Query: 469 APLVPPGTPVNNALAKQRAMLENIMRACVGLAPENNMILEYK 510. SEQ ID2
APLVPPGTPVNNALAKQRAMLENIMRACVGLAPENNMILEYK
Sbjct: 471 APLVPPGTPVNNALAKQRAMLENIMRACVGLAPENNMILEYK 512 SEQ ID3
CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total
secs.

Gapped
Lambda K H
0.316 0.134 0.385

Gapped
Lambda K H
0.267 0.0410 0.140

Matrix: BLOSUM62
Gap Penalties: Existence: 11, Extension: 1
Number of Hits to DB: 2125
Number of Sequences: 0
Number of extensions: 153
Number of successful extensions: 5
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's successfully gapped in prelim test: 0
Number of HSP's that attempted gapping in prelim test: 0
Number of HSP's gapped (non-prelim): 1
length of query: 510
length of database: 233,319,389
effective HSP length: 125
effective length of query: 385
effective length of database: 176,133,389
effective search space: 67811354765
effective search space used: 67811354765

Fig: 1 (Cont'd)